

ARTICLE

Open Access



Meta-analysis on the global prevalence of *Arcobacter* in food-producing animals and humans

Penghang Zhang^{1,2}, Yuzhu Liu¹, Mengjiao Fu², Bing Wang³, Shuangyang Ding⁴, Xiaochen Ma¹, Xiaoi Zhang^{1*} and Zhangqi Shen^{2,4*}

Abstract

The genus *Arcobacter* has been associated with illnesses in both animals and humans, where *Arcobacter butzleri*, *Arcobacter cryaerophilus*, and *Arcobacter skirrowii* have been linked to numerous cases of gastrointestinal diseases in humans. While isolated instances of *Arcobacter* infection have been reported in certain areas, comprehensive data reflecting the global impact of *Arcobacter* infection are lacking. This meta-analysis was conducted with the objective of assessing the aggregated prevalence of *Arcobacter* across diverse sources on a global scale. We conducted a thorough literature search of the Scopus, PubMed, and ScienceDirect databases to identify studies published from 1992 to 2022 on *Arcobacter* prevalence in humans and food-producing animals. We utilized multilevel random effects meta-analysis models to gauge the average occurrence of *Arcobacter* and to examine various factors that could influence incidence outcomes. Seventy-five articles were included in the meta-analysis. The pooled prevalence of *Arcobacter* spp. from different sources was 21.9% (95% CI: 18.0%–26.1%), and the mean prevalence of *A. butzleri*, *A. cryaerophilus*, and *A. skirrowii* was 15.1%, 2.8%, and 0.1%, respectively. *Arcobacter* spp. had the lowest prevalence in humans (1.8%; 95% CI: 0.7%–3.3%) and the highest in broilers (38.8%; 95% CI: 28.0%–50.1%). Among animal-derived food products, carcasses or carcass parts exhibited the highest *Arcobacter* spp. prevalence of 28.6% (28.6%; 95% CI: 23.7%–33.7%). This meta-analysis revealed that *A. butzleri* is the most prevalent *Arcobacter* species worldwide, with broilers, as well as seafood, being the primary hosts of *Arcobacter* spp. We recommend developing appropriate prevention strategies and conducting further local in-depth studies to establish the actual epidemiological burden of *Arcobacter*.

Keywords Meta-analysis, Prevalence, *Arcobacter* spp., Food-borne diseases

*Correspondence:

Xiaoi Zhang
zhangxiaoi_0922@163.com
Zhangqi Shen
szq@cau.edu.cn

¹Institute for Nutrition and Food Hygiene, Beijing Center for Disease Prevention and Control, Beijing, China

²National Key Laboratory of Veterinary Public Health and Safety, College of Veterinary Medicine, China Agricultural University, Beijing 100193, China

³Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, NE 68588, USA

⁴Beijing Key Laboratory of Detection Technology for Animal-Derived Food Safety, College of Veterinary Medicine, China Agricultural University, Beijing 100193, China

Introduction

Arcobacter spp. are considered important foodborne pathogens associated with both human and animal diseases [1]. The *Arcobacter* genus encompasses 29 identified species derived from various natural environments, including soil, freshwater, seawater, and hosts such as humans and animals [2–4]. Among these species, *Arcobacter butzleri*, *Arcobacter cryaerophilus* and *Arcobacter skirrowii* are clinically important for both animals and humans [5–7].

Poultry serves as a crucial reservoir for *Arcobacter* and a primary source of infection [8–10]. Poultry intestines, which harbor *Arcobacter*, can contaminate



© The Author(s) 2024. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

slaughterhouses during carcass processing, increasing the likelihood of further contamination [6]. Apart from poultry, *Arcobacter* has been recovered from various products of animal origin, including seafood, milk, beef, and pork [11–15]. Contaminated meat plays a crucial role in *Arcobacter* transmission [5, 16, 17]. In humans, severe illnesses, such as peritonitis, endocarditis, bacteremia, and prolonged watery gastroenteritis with abdominal cramps, have been reported following *Arcobacter* infection [18, 19]. Given the absence of daily diagnostic methods specifically designed for *Arcobacter* spp. detection, the importance and prevalence of infections are possibly underestimated. In a recent study, *Arcobacter* prevalence in diarrhea individuals and in raw chickens was 1.3% and 26.7%, respectively, in China [1]. Conversely, in Germany, *Arcobacter* is the second most prevalent bacterial pathogen detected in human stool samples, while in Belgium, it is the fourth most prevalent [5, 20].

To date, only a limited number of studies have investigated *Arcobacter* prevalence in both humans and food-producing animals on a global scale. Meta-analysis serves as the invaluable statistical methodology with the objective of synthesizing, integrating, and contrasting results from numerous primary studies investigating the same questions; it is essential when quantitative comparisons worldwide are necessary. In this study, we employed meta-analysis to quantitatively summarize and compared the prevalence of *Arcobacter* in humans and food-producing animals globally, providing a foundation for future *Arcobacter* disease surveillance.

Results

Excluded studies

The literature study identified 1142 scientific papers containing the terms "prevalence" or "incidence" along with "*Arcobacter*." The exclusion criteria included reviews, duplicated studies or data, investigations concentrating solely on laboratory techniques, and studies lacking adequate data for estimating *Arcobacter* prevalence ($n=1027$; Fig. 1).

Included studies

Out of the 1142 scientific papers screened, seventy-five met all the inclusion criteria for estimating *Arcobacter* spp. prevalence, encompassing 176 prevalence studies. Additionally, 167, 145, and 136 studies evaluating the prevalence of *Arcobacter butzleri*, *Arcobacter cryaerophilus* and *Arcobacter skirrowii*, respectively, were included.

Among all studies estimating *Arcobacter* spp. prevalence, a notable majority were published in the period after 2006 (Fig. 2). After 2006, there was an increase in studies involving *Arcobacter* species, particularly with a greater focus on *A. butzleri* than on *A. cryaerophilus*

or *A. skirrowii*. These studies were conducted across 34 different countries on 6 continents, with the majority located in Europe and Asia (Fig. 2).

Thermotolerant *Arcobacter* prevalence

Among the 75 scientific papers meeting the inclusion criteria, we identified 176 studies on the prevalence of *Arcobacter* spp. (analyzing 76,951 samples). From these 176 studies, the combined prevalence estimate for *Arcobacter* spp. was 21.9% (95% CI: 18.0%–26.1%). Notably, significant heterogeneity was detected across the studies (Q-statistic: $p < 0.0001$; I^2 -statistic = 98.91%).

A total of 167 studies on *A. butzleri* prevalence were selected (76,525 samples were analyzed). The prevalence estimate for *A. butzleri* was 15.1% (95% CI: 12.4%–18.5%), and notable heterogeneity was detected (Q-statistic: $p < 0.0001$; I^2 -statistic = 98.51%).

We identified 145 studies on the prevalence of *A. cryaerophilus* (analyzing 72,516 samples). The prevalence estimate for *A. cryaerophilus* was 2.8% (95% CI: 1.7%–4.1%), with notable heterogeneity detected (Q-statistic: $p < 0.0001$; I^2 -statistic = 95.69%).

Finally, 136 studies on *A. skirrowii* prevalence were identified (comprising 71,673 samples), with a prevalence estimate of 0.1% (95% CI: 0.0%–0.4%). Significant heterogeneity was observed across these 136 studies (Q-statistic: $p < 0.0001$; I^2 -statistic = 80.43%).

Evolution of *Arcobacter* prevalence over the analyzed period

In this meta-analysis, we opted to focus on publication year rather than the year of the study. This decision was based on the conventional alignment between the publication year of scientific articles and the actual year of study, which typically falls within a range of 2 to 3 years.

Arcobacter spp. prevalence within all humans and food-producing animals included in this meta-analysis varied based on publication year (Fig. 3a). The prevalence ranged from 0.064 to 0.273 over the analyzed period. The highest prevalence appeared within published studies from 2006 to 2010 (27.3%; 95% CI: 18.1%–37.5%; $p < 0.001$). This pattern remained consistent when considering the prevalence among bivalves, bovines, and cows. Cumulative analysis and meta-regression analysis revealed no evidence of a shift in prevalence over time (Table 1) for all *Arcobacter* spp. or for either subtype reviewed.

A. butzleri prevalence within all humans and food-producing animals included in this meta-analysis varied depending on the study publication year (Fig. 3b). The highest prevalence was noted within published studies during 2001–2005 (25.3%; 95% CI: 6.3%–50.6%;

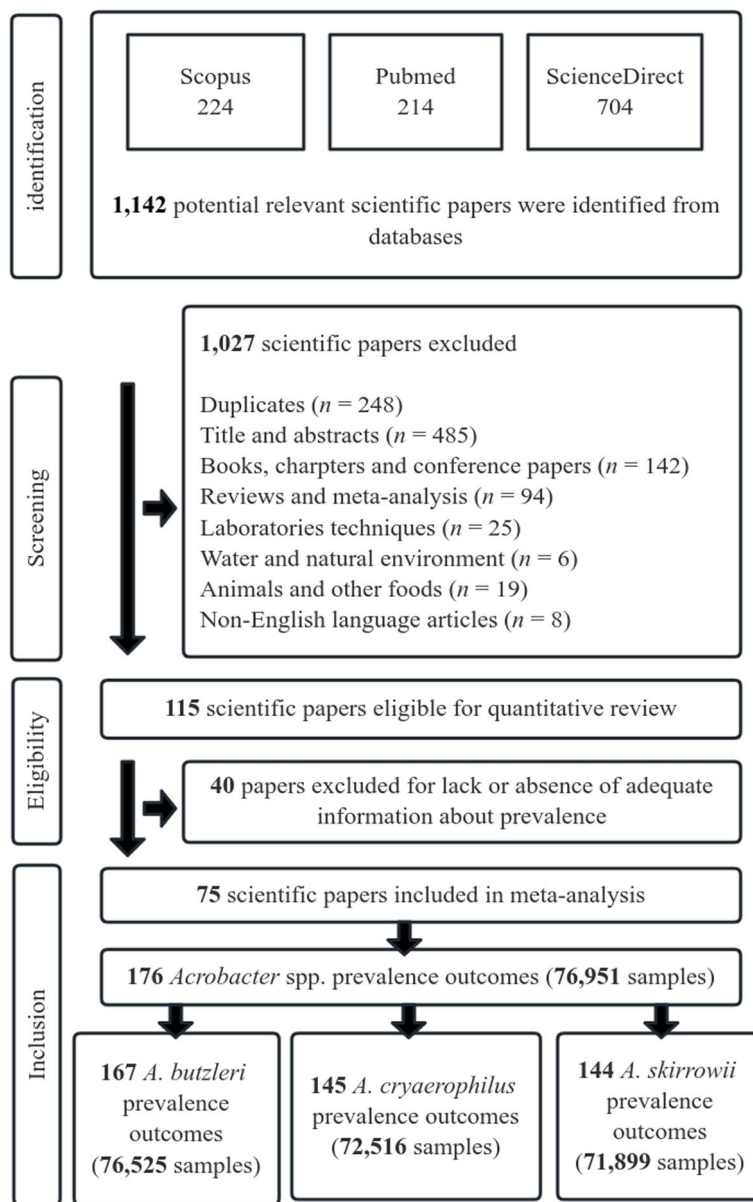


Fig. 1 Flowchart depicting the study selection process for inclusion within meta-analysis

$p < 0.001$), while the prevalence of *A. butzleri* ranged from 4.6% to 25.3% throughout publication years (Table 1).

In comparison to discovered all *Arcobacter* spp. prevalences and *A. butzleri*, *A. cryaerophilus* and *A. skirrowii* prevalence in all humans and food-producing animals included in the meta-analysis was low, with no isolation data available before 2000 (Fig. 3c and d). *A. cryaerophilus* and *A. skirrowii* prevalence ranged from 1.8% to 5.8% and from 0.0% to 0.8%, respectively, throughout the years of publication. The highest prevalence of *A. cryaerophilus* was observed during

2006–2010 (5.8%; 95% CI: 2.0%–10.8%; $p < 0.001$), and for *A. skirrowii*, it was during 2011–2015 (0.8%; 95% CI: 0.2%–1.7%; $p < 0.001$).

Prevalence of *Arcobacter* across different regions

North America-located studies (33.0%; 95% CI: 8.6%–63.8%) and South America studies (29.8%; 95% CI: 13.5%–49.0%) detected the highest *Arcobacter* spp. prevalence ($p < 0.001$), with highest prevalence found in other birds (85.4% and 55.7%, respectively). Moreover, the lowest *Arcobacter* spp. prevalence. was observed in Asia (16.6%; 95% CI: 11.9%–21.8%) and

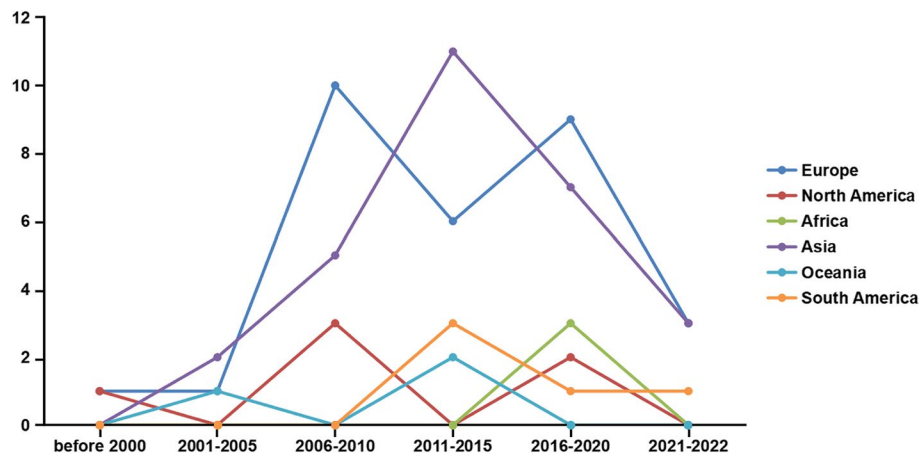


Fig. 2 Distribution of studies included in the meta-analysis on *Arcobacter* spp., categorized by year of publication and continent

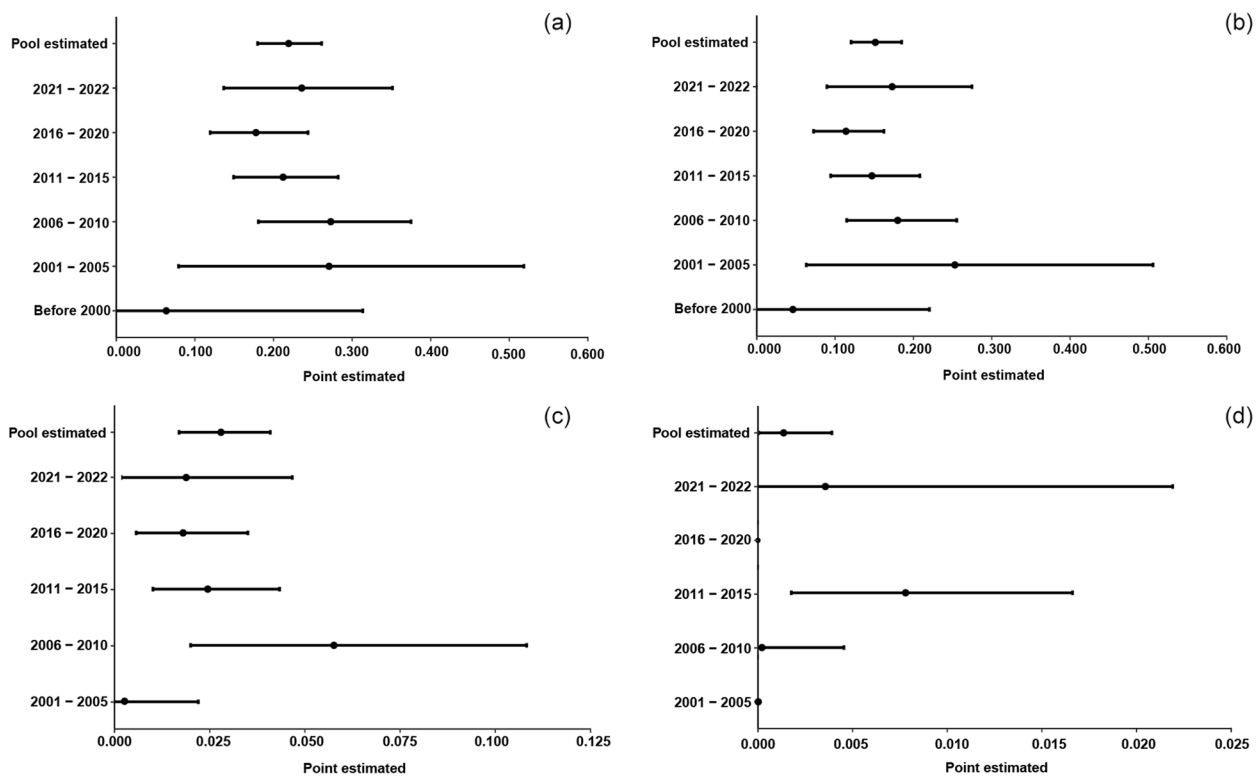


Fig. 3 Subgroup analysis comparing *Arcobacter* prevalence over years in food-producing animals and humans. **a** *Arcobacter* spp.; **b** *Arcobacter butzleri*; **c** *Arcobacter cryaerophilus*; **d** *Arcobacter skirrowii*

Africa (17.0%; 95% CI: 9.1%–26.8%; Fig. 4a). *Arcobacter* spp. prevalence in broilers surpassed that in Oceania countries (72.7%; 95% CI: 51.9%–89.6%; $n = 22$), South America (69.7%; 95% CI: 62.7%–76.3%; $n = 175$), Europe (47.4%; 95% CI: 24.0%–71.4%; $n = 1499$), and North America (35.5%; 95% CI: 6.9%–71.8%; $n = 1002$) than

in the countries of Asia (33.0%; 95% CI: 20.1%–47.3%; $n = 1956$) and Africa (17.7%; 95% CI: 5.0%–35.9%; $n = 450$). However, the prevalence in humans was lower in Europe (0.7%; 95% CI: 0.2%–1.4%; $n = 54,147$), South America (0.9%; 95% CI: 0.0%–3.5%; $n = 339$), Oceania (1.2%; 95% CI: 0.7%–1.8%; $n = 1380$), Asia (2.1%; 95%

Table 1 Overview of Random weighted meta-regression analysis

<i>Arcobacter</i> specie	Intercept ^a	Slope	P-value
<i>Arcobacter</i> spp.	0.5224	-0.0067	0.7519
<i>Arcobacter butzleri</i>	0.4515	-0.0102	0.5876
<i>Arcobacter cryaerophilus</i>	0.2929	-0.0226	0.1457
<i>Arcobacter skirrowii</i>	0.1270	-0.0056	0.4797

The table provides a concise overview of the random weighted meta-regression analysis. It examines the relationship between the year of publication, treated as the independent variable, and the prevalence of *Arcobacter* isolates from food-producing animals, which serves as the outcome variable

^a Intercept: constant in the model

CI: 0.3%–5.0%; $n = 3748$), and North America (2.9%; 95% CI: 0.0%–9.7%; $n = 1703$) than in Africa (15.8%; 95% CI: 12.8%–19.2%; $n = 505$).

Studies located within countries of Oceania and North America identified the highest *A. butzleri* prevalence ($p < 0.001$; Fig. 4b), while Oceania, South America, and Europe had the highest *A. cryaerophilus* prevalence ($p < 0.001$; Fig. 4c). Africa and Asia had the lowest *A. butzleri* and *A. cryaerophilus* prevalence. *A. skirrowii* prevalence in Oceania was 3.2% (95% CI: 0.0%–25.3%; $p < 0.001$; Fig. 4d) compared to the

close-to-zero prevalence rate of *A. skirrowii* in other continents.

Prevalence of *Arcobacter* in human stools and food-producing animal species

Arcobacter spp. prevalence in humans (1.8%; 95% CI: 0.7%–3.3%; $p < 0.001$; Fig. 5a) was significantly lower than that in food-producing animal species. Similar results were observed when independently analyzing the prevalence of *A. butzleri*, *A. cryaerophilus* and *A. skirrowii* (Fig. 5b and d). Broilers exhibited the highest prevalence of *Arcobacter* spp. (38.8%; 95% CI: 28.0%–50.1%), followed by seafood such as bivalves (35.4%; 95% CI: 24.0%–47.6%) and fish (33.1%; 95% CI: 14.6%–54.4%). In contrast, among the sampled food-producing animals, goats and ovines presented the lowest prevalence (9.6%; 95% CI: 1.2%–23.7%). Broilers and fish samples also exhibited the highest *A. butzleri* prevalence ($p < 0.001$), while the greatest *A. cryaerophilus* and *A. skirrowii* prevalence was observed in bivalves.

Prevalence of *Arcobacter* within various types of food samples

This subgroup analysis excluded human stool samples. The highest *Arcobacter* spp. prevalence was detected when specimens were collected from carcasses or parts of

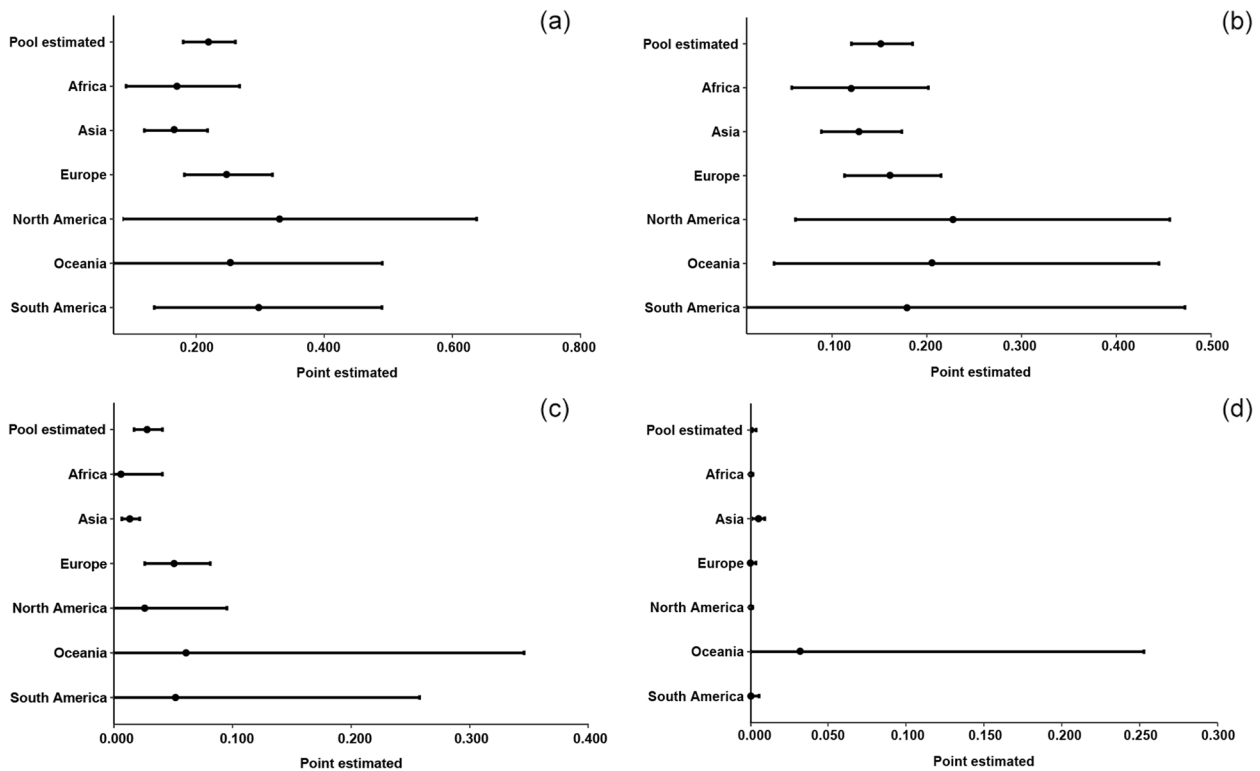


Fig. 4 Subgroup analysis comparing *Arcobacter* prevalence across continents in food-producing animals and humans. **a** *Arcobacter* spp.; **b** *Arcobacter butzleri*; **c** *Arcobacter cryaerophilus*; **d** *Arcobacter skirrowii*

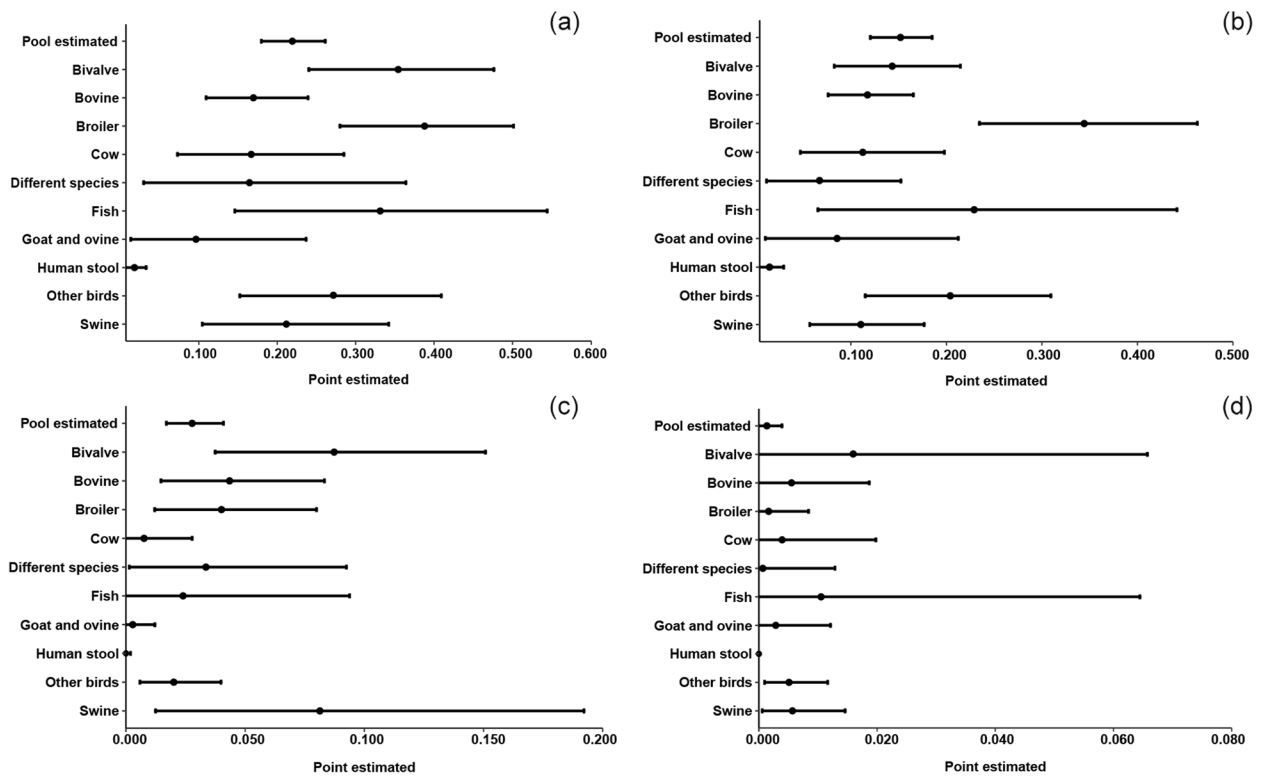


Fig. 5 Subgroup analysis comparing *Arcobacter* prevalence across food-producing animals and humans. **a** *Arcobacter* spp.; **b** *Arcobacter butzleri*; **c** *Arcobacter cryaerophilus*; **d** *Arcobacter skirrowii*

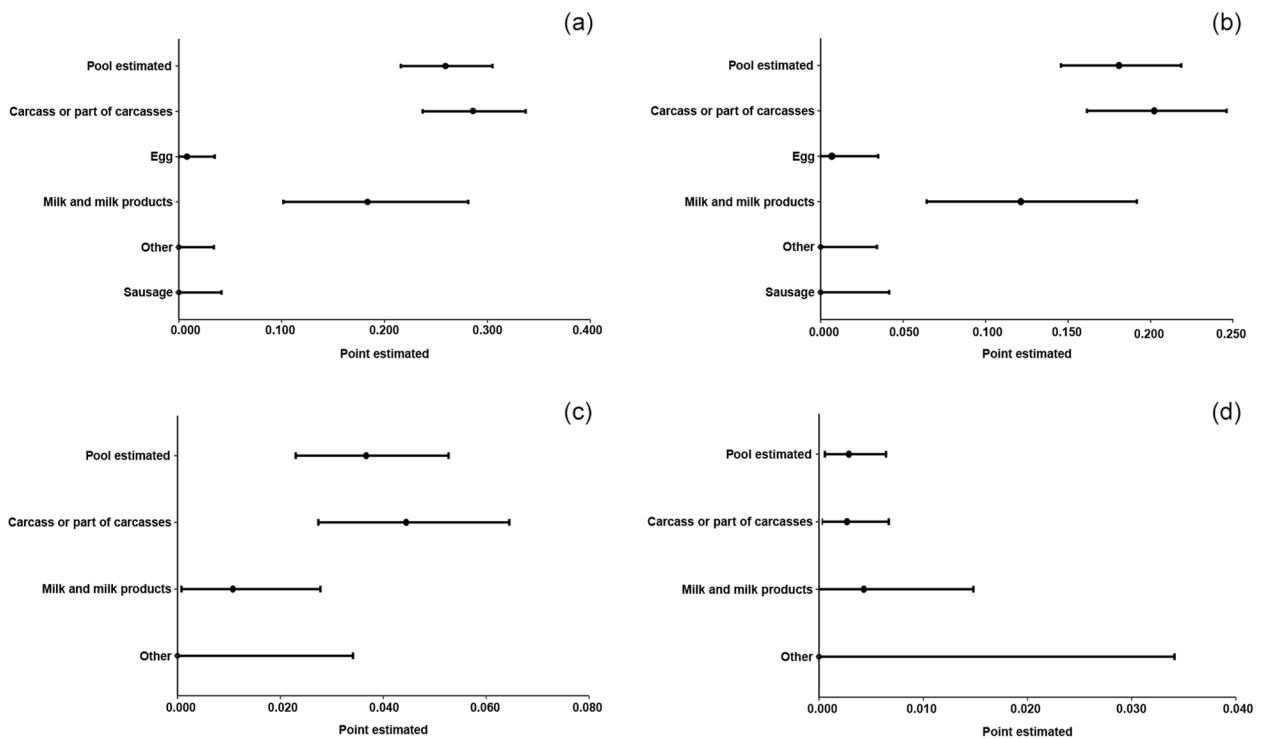


Fig. 6 Subgroup analysis comparing *Arcobacter* prevalence based on sample type. **a** *Arcobacter* spp.; **b** *Arcobacter butzleri*; **c** *Arcobacter cryaerophilus*; **d** *Arcobacter skirrowii*

carcasses (28.6%; 95% CI: 23.7%–33.7%; Fig. 6a) and milk and milk products (18.3%; 95% CI: 10.2%–28.1%). However, there were no reports of *Arcobacter* spp. positive detection in sausages or other foods. Similar results were observed when analyzing *A. butzleri*, *A. cryaerophilus* and *A. skirrowii* prevalence individually (Fig. 6b and d).

Prevalence of *Arcobacter* considering storage time and method

When samples were stored using any freezing method or stored (refrigerated or ambient) for 2–7 days before *Arcobacter* isolation, the prevalence of *Arcobacter* spp. was lower than that with other storage and sampling practices. In contrast, when samples were refrigerated or *Arcobacter* was isolated on the same day or after overnight storage, the prevalence of *Arcobacter* spp. was higher (Fig. 7a). Samples kept in ambient storage showed a higher prevalence of *Arcobacter* spp. than those kept in refrigerated storage when bacteria were isolated on the same day ($p < 0.001$). In contrast, there was a greater *Arcobacter* spp. prevalence among samples kept in refrigerated storage overnight than those in ambient storage overnight ($p = 0.033$). However, when samples were stored for 2–7 days, ambient or refrigerated storage had no influence on *Arcobacter* spp. prevalence rate ($p = 0.270$).

Studies involving the same-day *Arcobacter* spp. collected from samples stored under ambient conditions illustrated the highest *A. butzleri* prevalence ($p < 0.001$; Fig. 7b); however, this was only verified in swine. The highest *A. cryaerophilus* and *A. skirrowii* prevalence was observed in refrigerated samples, followed by refrigerated samples when bacteria were isolated after storage overnight (Fig. 7c, d).

Prevalence of *Arcobacter* considering isolation method

We compared the prevalence of *Arcobacter* spp. based on whether a membrane filter was utilized on the selective medium. The prevalence of *Arcobacter* spp. (25.5%; 95% CI: 19.4%–32.2%; $n = 50,274$; Fig. 8a) was higher in studies that used a membrane filter on selective media than in those that used selective media without a membrane filter (19.3%; 95% CI: 14.3%–24.8%; $n = 26,427$; $p < 0.001$). Reports not specifying the isolation method indicated the lowest prevalence rate (10.4%; 95% CI: 6.9%–14.5%; $n = 250$). Similar results were observed when analyzing *A. cryaerophilus* and *A. butzleri* prevalence independently (Fig. 8b and c). However, the prevalence of *A. skirrowii* (0.1%; 95% CI: 0.0%–0.5%; Fig. 8d) was lower in studies that used a membrane filter on selective media than in those that used selective media

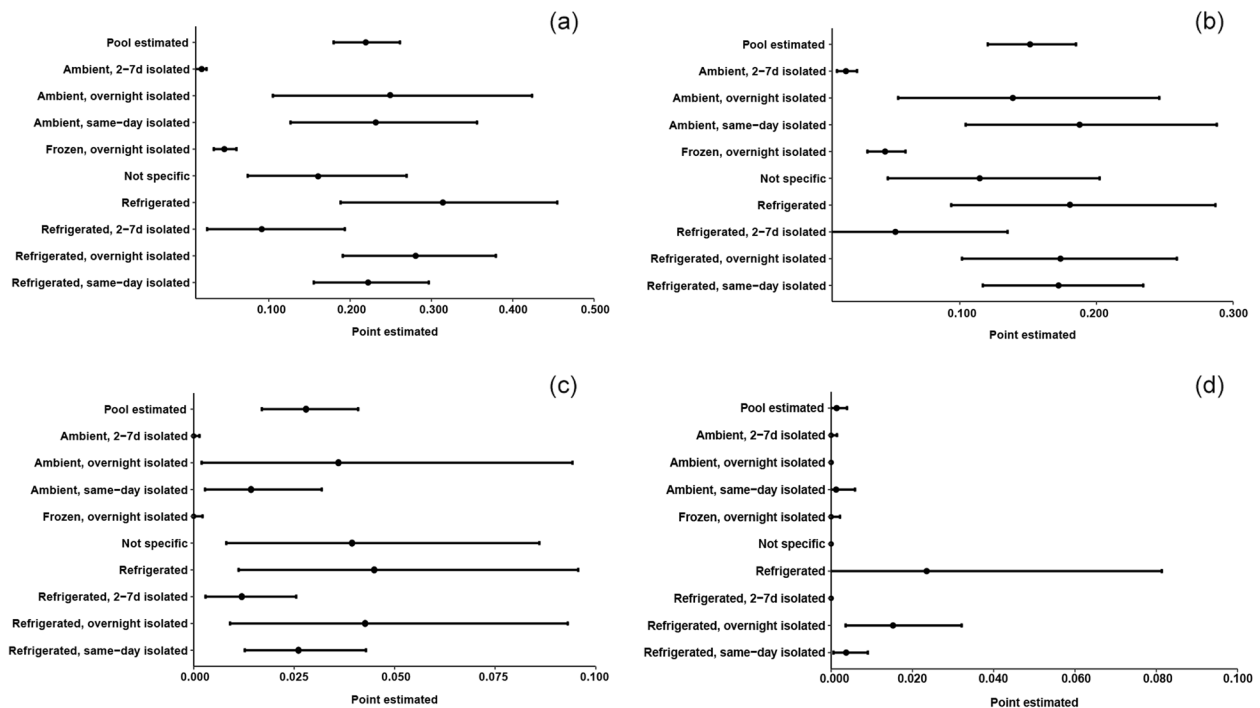


Fig. 7 Subgroup analysis comparing *Arcobacter* prevalence considering the storage method. **a** *Arcobacter* spp.; **b** *Arcobacter butzleri*; **c** *Arcobacter cryaerophilus*; **d** *Arcobacter skirrowii*

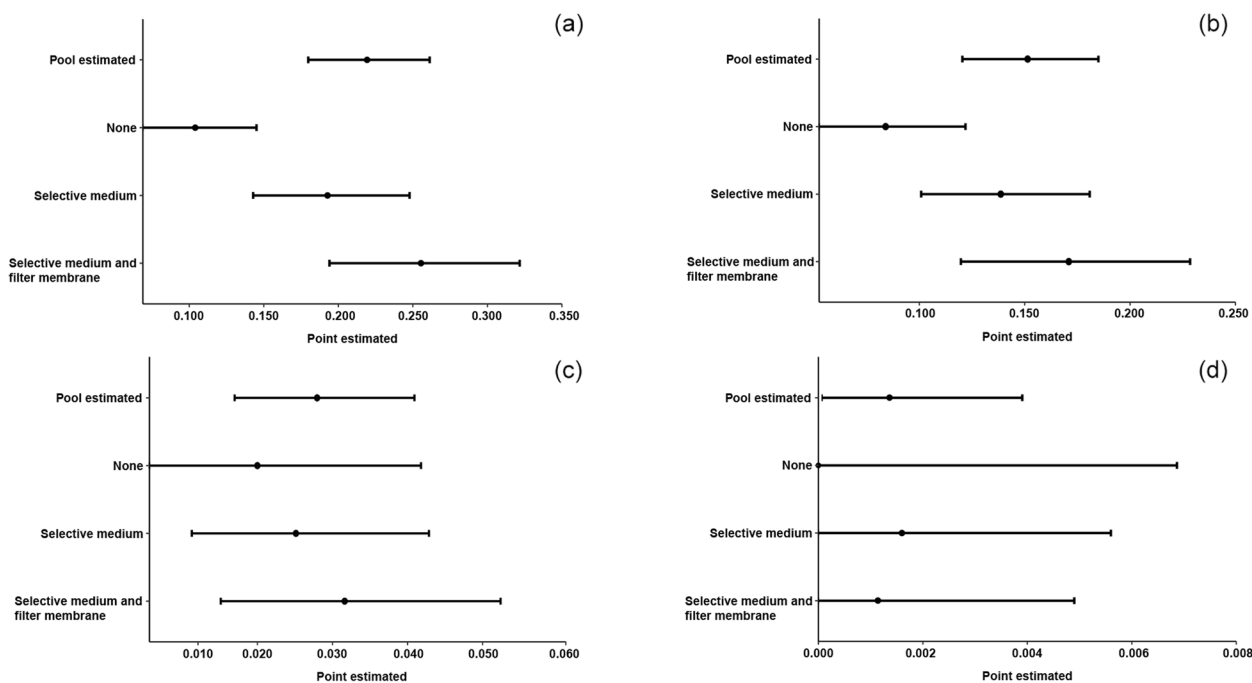


Fig. 8 Subgroup analysis comparing *Arcobacter* prevalence considering the isolation method. **a** *Arcobacter* spp.; **b** *Arcobacter butzleri*; **c** *Arcobacter cryaerophilus*; **d** *Arcobacter skirrowii*

Table 2 Outcomes of publication bias detection outcomes

Response variable	Fail-safe N ^a	Begg and Mazumdar test	Egger’s regression test	
			Intercept	P-value
<i>Arcobacter</i> spp.	0	0.0479	7.6681	0.0154
<i>Arcobacter butzleri</i>	0	0.1043	6.4018	0.0134
<i>Arcobacter cryaerophilus</i>	0	0.1313	3.1552	0.0088
<i>Arcobacter skirrowii</i>	0	<0.0001	1.9141	0.0034

^a Research quantity needed to reverse the effects is computed based on a significance level of $P=0.05$

without a membrane filter (0.2%; 95% CI: 0.0%–0.6%; $p < 0.001$).

Publication bias

None of the individual studies significantly influenced the summary prevalence estimate of *Arcobacter*, as indicated by sensitivity and cumulative analyses.

To assess publication bias among the included studies, we employed Egger’s regression test, the Begg and Mazumdar rank correlation test, and the fail-safe N method, as detailed in Table 2. Our findings revealed a prevalent tendency toward publication bias across most *Arcobacter* species. Nonetheless, the extensive inclusion of scientific articles in this meta-analysis ensures

the validity of our results, mitigating the impact of potential bias.

Discussion

Arcobacter spp. are significant pathogens of growing interest for public health and food safety due to their frequent detection in various foods and the clinical relevance of *A. butzleri*, *A. cryaerophilus* and *A. skirrowii* in humans [5]. Consequently, over the last decade, the number of studies investigating the prevalence and incidence of *Arcobacter* in both humans and food-producing animals has increased [1, 4, 7, 13, 14]. We analyzed *Arcobacter* spp. presence within humans and various animal food products globally. According to the meta-analysis, approximately 21.9% of the samples analyzed contained *Arcobacter*: 1.80% in human stools and 25.9% in animal food products, regardless of the animal species. Among *Arcobacter* spp., *A. butzleri* served as the dominant type, while the prevalence of *A. skirrowii* and *A. cryaerophilus* was low. This discovery holds significant importance because it underscores the widely acknowledged transmission route of pathogens through the food chain, particularly notable for *A. butzleri*, a primary causative agent of human *Arcobacter* disease [20].

Although our study did not reveal a surge in *Arcobacter* prevalence across the years, numerous reports have highlighted a growing number of human *Arcobacter* disease cases globally [1, 4, 16]. This trend might be attributed

to data stemming from outbreaks or epidemiological studies, which could introduce biases, particularly regarding unreported cases. An increase in case reporting could inflate prevalence estimates without necessarily reflecting an increase in disease incidence. Conversely, the heightened incidence of human *Arcobacter* disease might stem from enhanced surveillance and identification of microbial agents responsible for foodborne illnesses previously categorized as acute gastroenteritis [21, 22].

The prevalence of *Arcobacter* varies across continents. Africa and Asia exhibit the lowest prevalence of *Arcobacter* spp., but an exceptionally high prevalence is observed in human stools in Africa. This phenomenon may be linked to the dietary and hygiene habits prevalent in developing countries. Higher prevalence of *Arcobacter* has been reported in animal food samples (25.9%) than in human samples, likely because most domestic animals can serve as reservoirs for *Arcobacter*. Notably, we detected a greater prevalence of *Arcobacter* in North America and South America than in other continents, especially in other birds, predominantly turkey. Poultry seems to be a crucial host for *Arcobacter*, similar to *Campylobacter* [23].

Furthermore, poultry intestines frequently incur damage during slaughter, leading to the contamination of carcasses with pathogens. In contrast, the slaughter processes for other species, such as cattle and swine, are typically more tightly controlled to mitigate the risk of intestinal perforation. This meta-analysis also identified broilers as the most pivotal *Arcobacter* source, highlighting the significance of poultry in the global transmission of *Arcobacter* [24]. Numerous investigations have reported the persistence and diffusion of *Arcobacter* in poultry meat [25–27] and seafood [28–30] production chains.

Numerous *Arcobacter* species are recognized as indigenous to aquatic habitats, whereas the occurrence of *A. cryaerophilus*, *A. skirrowii*, *A. butzleri*, might be linked to fecal contamination of water bodies originating from animal waste [29]. Given their filter-feeding ability, marine bivalve mollusks can accumulate bacterial pathogens from water sources, thereby posing a substantial health risk to consumers, particularly when consumed raw or undercooked [31]. This phenomenon could elucidate the elevated prevalence of *Arcobacter* spp. observed in seafood as reported in this meta-analysis.

Arcobacter spp. can be transmitted to humans through routes other than those involving meat. An *Arcobacter* outbreak has been linked to the consumption of milk [32]. *Arcobacter* presence within milk typically results from fecal contamination within the milking procedure [33], potentially leading to human infection in cases of

incomplete sterilization or post-pasteurization cross-contamination. *Arcobacter* prevalence in milk and milk products was 18.3%, indicating that this genus is another significant source of contamination. Similarly, eggs, sausages, and other foods showed a low prevalence of *Arcobacter* spp., suggesting a lower likelihood of causing infection in humans. Despite originating from the same animals, the environment in which these products are sourced and stored can significantly impact *Arcobacter* prevalence.

Furthermore, this meta-analysis investigated the impact of storage time and method on *Arcobacter* prevalence. We detected a higher *Arcobacter* spp. prevalence in samples stored refrigerated or isolated on the same day or after overnight storage than in samples stored via other methods. When bacteria were isolated on the day of sample collection, the prevalence rate was highest when the samples were stored at ambient temperature. On the second day after sample collection, refrigerated storage resulted in the highest *Arcobacter* isolation rate. However, for food safety considerations, long-term frozen storage has emerged as an effective method for reducing the survival of *Arcobacter* spp. Studies also indicate that freezing affects the isolation rate of both *Campylobacter* and *Arcobacter* [34, 35].

This meta-analysis facilitated a comparison of the prevalence with and without the use of a membrane filter on selective medium. The filtration method, which was originally developed for detecting *Campylobacter* in clinical human stool specimens containing a high concentration of background bacteria [36], has been gradually applied in the isolation of *Campylobacter* in food [37]. In 2019, the Chinese Preventive Medicine Association included the membrane filter method in the group standard for identifying *Campylobacter jejuni* and *Campylobacter coli* [38]. Moreover, membrane filters have been utilized in many studies to isolate *Arcobacter* [4, 13, 14, 28, 39]. Our meta-analysis revealed a higher prevalence of *Arcobacter* spp. when membrane filters were used than when membrane filters were not used, demonstrating that the use of membrane filters is an effective method for improving the isolation rate of *Arcobacter*.

We acknowledge some limitations to our study. The meta-analysis is limited by heterogeneity among studies and potential publication bias. Differences in study design and quality can affect the reliability of synthesized results. Publication bias may lead to an overrepresentation of studies with significant findings, overlooking those with lower prevalence rates or nonsignificant outcomes.

Food-producing animals stand out as the most crucial reservoirs and sources of *Arcobacter*, posing a serious challenge for public health in terms of pathogen transmission from farm to table [40, 41]. Subsequent research endeavors

should prioritize the epidemiology and transmission of *Arcobacter*, particularly in food production. Investigating effective prevention and control measures is crucial for reducing *Arcobacter* transmission along the food chain, enhancing food safety and public health. Consequently, we advocate for stricter food safety control strategies by food manufacturers to prevent *Arcobacter* contamination in food. Simultaneously, we propose the inclusion of *Arcobacter* in international or national food safety monitoring systems to determine appropriate risk assessment measures aimed at curbing the prevalence of *Arcobacter* and the resulting *Arcobacter* disease in humans.

Conclusion

The meta-analysis revealed a pooled prevalence of 21.9% for *Arcobacter* spp., showing a higher prevalence in animal food samples, with *A. butzleri* emerging as the predominant species. Varied prevalence levels of *Arcobacter* were detected in humans and food-producing animals across different regions. Notably, some food-producing animals, particularly broilers, bivalves, and fish, exhibited a higher prevalence of *Arcobacter* than others. *A. butzleri* demonstrated higher prevalence in broilers and lower prevalence in goats, ovines, and swines. Conversely, *A. cryaerophilus* and *A. skirrowii* were predominantly found in bivalves.

This meta-analysis further highlighted a substantial prevalence of *Arcobacter* spp. in animal food products, particularly in carcasses and parts of carcasses from diverse animal species and in milk and milk products. Egg products and processed meat items, such as sausages, did not emerge as significant *Arcobacter* spp. sources. Moreover, although refrigeration is widely acknowledged as a method for food preservation, it seems to have little impact on reducing *Arcobacter* spp. prevalence in animal food products. The use of membrane filters on selective media influenced the amount of *Arcobacter* spp. detected.

In light of these findings, it is imperative for researchers to swiftly devise tools aimed at diminishing the prevalence of *Arcobacter* in primary production, disrupting its fecal–oral cycle, particularly in intensive production systems.

Materials and methods

Data sources

Scientific papers published in English since the *Arcobacter* spp. via the nomenclature were identified through comprehensive searches of the Scopus, PubMed, and ScienceDirect databases. The search terms for each database included "prevalence" or "incidence" and "*Arcobacter*." Abstracts and titles were meticulously evaluated, and articles that adhered to the predetermined inclusion criteria were chosen. Data extraction from the selected studies was carried out independently by two authors. In

instances of disagreement, resolution transpired through discussions between the two reviewers and thorough examination of the trial information. If necessary, contact with the trial authors was established to seek clarification.

Criteria for study selection

The evaluation of scientific articles for inclusion in the meta-analysis involved several stages. Initially, articles were screened for adherence to selection criteria, with a focus on identifying duplicates, reviews, studies involving humans, animals, and foods, as well as diagnostic methodology validations. Each scientific article underwent a thorough examination, with a specific focus on extracting the statistical data necessary for meta-analysis. Furthermore, the references cited within these articles were scrutinized to identify any additional relevant studies that met the selection criteria. The data were extracted by one author and independently verified by another investigator.

The following eligibility criteria for the inclusion of scientific papers included within the meta-analysis were outlined: (1) Observational study design, specifically prevalence studies. (2) Publication in peer-reviewed journals.

In instances where a scientific paper included humans, different animal species, and food, each animal was treated as an individual "study" within the meta-analysis. Likewise, if a scientific paper reported findings under different circumstances (such as country of origin, sample type, or methodology for confirming *Arcobacter* spp.), each circumstance was treated as an individual study. As a result, one scientific paper could contribute multiple studies to the analysis.

For inclusion, studies needed to provide data on both the total sample size (population) and sample quantity that tested positive for *Arcobacter*. *Arcobacter* spp. identification relies on typical morphology, biochemical confirmation, or, in some instances, PCR detection. Whenever possible, details regarding *Arcobacter* species identification were incorporated into the analysis.

Exclusions from the meta-analysis encompassed various criteria such as assorted reviews, duplicate reports, non-peer-reviewed articles (e.g., theses, opinion articles, conference papers, and letters to editors), articles not in English, and those describing *Arcobacter* detection within artificially contaminated specimens. Additionally, articles involving direct PCR identification without bacterial culture experiments or focusing solely on laboratory techniques were excluded.

Outcomes and definitions

The prevalence of the genus *Arcobacter* and its constituent species (*A. skirrowii*, *A. butzleri*, and *A. cryaerophilus*.) was determined by calculating the ratio of positive samples to the total number of samples. The

study population included humans and various food-producing animal species investigated in each study. A pivotal criterion for differentiation was the concept of harvesting, serving as the delineation between animal samples and food samples. Notably, samples derived from animal feces and swabs were excluded from the classification of food samples (i.e., this study).

Data extraction

Details encompassing the study design, country, years under consideration, isolate source, sample type, origin of samples, sample storage method, methodology employed for bacterial isolation and confirming *Arcobacter* identity, and outcomes (including the number of positive *Arcobacter* samples and the total sample count for humans, animals, or food) were meticulously extracted from each research paper. Notably, the exclusion of studies did not rely on the utilization of scores [42].

Quality assessment

Two authors autonomously evaluated the risk of bias in each original study. The quality of each study was evaluated utilizing the Newcastle–Ottawa scale, which was adapted for cross-sectional studies [43], and grades ranging up to 10 points. This tool comprises three key sections: methodological quality (8 points), comparability of the study (1 point), and outcomes related to statistical analysis (1 point). The final decision was based on the mean score from the two authors, and studies with a score equal to or greater than five were deemed eligible for meta-analysis and systematic review (Table S1).

Statistical analysis and subgroup analysis

Statistical analysis was performed utilizing Comprehensive Meta-Analysis version 2.2 (2011). Given the binary nature of the measured outcome (i.e., whether human, food-producing animal, or food samples tested positive or negative for the pathogen) and its reporting solely for individual groups, the most applicable parameter for effect size measurement was the raw proportion 'p' (accompanied by 95% CIs) utilizing a random-effects model [44]. Heterogeneity among studies was assessed utilizing the DerSimonian and Laird test (Q-statistic). The extent of heterogeneity was quantified using the inconsistency index (I^2 -statistic) [45].

To assess the impact of outliers or highly influential studies on the analysis outcome, sensitivity analyses were conducted [42]. This process entailed iteratively performing the same analysis while excluding one study in each iteration. Furthermore, a cumulative meta-analysis was performed to evaluate how the outcomes varied with the publication year.

Subgroup analyses were preplanned to investigate potential factors influencing *Arcobacter* prevalence: (1) continent (geographic distribution), (2) human stool and food-producing animal species, (3) food types (sausages; other food product samples; milk and milk products; carcasses or part of carcasses; eggs), (4) storing time and methodology (isolation the same day or after overnight or storage for 2–7 days; ambient, refrigerated, or frozen), and (5) methodology for isolation (selective medium; selective medium plus filter) and identification of *Arcobacter* species. In the subgroup analysis for the time period considered, publication year was used instead of the study year. Typically, the publication year of a scientific article closely aligns with the study year (within 2 or 3 years).

Furthermore, a meta-regression analysis was conducted to investigate sources of heterogeneity by examining the association between *Arcobacter* prevalence and publication year, employing the method of moments. To assess the significance of covariates and measure the strength of their relationship with effect size, an index based on the percentage reduction in true variance was employed, similar to the R2 index utilized in primary studies [44].

Publication bias was assessed through the use of funnel plots. Adjusted rank correlation tests, the Egger method [46], Begg's test [47], and the fail-safe N method were used to assess publication bias.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s44280-024-00046-y>.

Supplementary Material 1.

Acknowledgements

Not applicable.

Authors' contributions

P.Z. and Y.L. performed data extraction, while P.Z. and M.F. established the research selection criteria. P.Z., X.M., and B.W. conducted the statistical and subgroup analysis. S.D., Z.S. and X.Z. provided guidance for this study. All authors read and approved the final manuscript.

Funding

This work was supported by the National Natural Science Foundation of China (Grant No. 32225048) and the Capital High-level Public Health Technical Talent Development Project (2022–3–027).

Availability of data and materials

Not applicable.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Received: 28 January 2024 Revised: 25 March 2024 Accepted: 28 March 2024

Published online: 10 May 2024

References

- Wang YY, Zhou GL, Li Y, Gu YX, He M, Zhang S, et al. Genetic characteristics and antimicrobial susceptibility of *Arcobacter butzleri* isolates from raw chicken meat and patients with diarrhea in China. *Biomed Environ Sci*. 2021;34(12):1024–8.
- Fernandez H, Villanueva MP, Mansilla I, Gonzalez M, Latif F. *Arcobacter butzleri* and *A. cryaerophilus* in human, animals and food sources, in southern Chile. *Braz J Microbiol*. 2015;46(1):145–7.
- Niedermeier JA, Miller WG, Yee E, Harris A, Emanuel RE, Jass T, et al. Search for *Campylobacter* spp. reveals high prevalence and pronounced genetic diversity of *Arcobacter butzleri* in floodwater samples associated with hurricane Florence in North Carolina, USA. *Appl Environ Microb*. 2020;86(20):e01118–20.
- Uljanovas D, Gözl G, Brückner V, Grineviciene A, Tamuleviciene E, Alter T, et al. Prevalence, antimicrobial susceptibility and virulence gene profiles of *Arcobacter* species isolated from human stool samples, foods of animal origin, ready-to-eat salad mixes and environmental water. *Gut Pathog*. 2021;13(1):76.
- Brückner V, Fiebiger U, Ignatius R, Friesen J, Eisenblätter M, Höck M, et al. Prevalence and antimicrobial susceptibility of *Arcobacter* species in human stool samples derived from out- and inpatients: the prospective German *Arcobacter* prevalence study Arcopath. *Gut Pathog*. 2020;12:21.
- Khodamoradi S, Abiri R. The incidence and antimicrobial resistance of *Arcobacter* species in animal and poultry meat samples at slaughterhouses in Iran. *Iran J Microbiol*. 2020;12(6):531–6.
- Vidal-Veuthuy B, Jara R, Santander K, Mella A, Ruiz S, Collado L. Antimicrobial resistance and virulence genes profiles of *Arcobacter butzleri* strains isolated from back yard chickens and retail poultry meat in Chile. *Lett Appl Microbiol*. 2021;72(2):126–32.
- Dekker D, Eibach D, Boahen KG, Akenten CW, Pfeifer Y, Zautner AE, et al. Fluoroquinolone-resistant *Salmonella enterica*, *Campylobacter* spp., and *Arcobacter butzleri* from local and imported poultry meat in Kumasi, Ghana. *Foodborne Pathog Dis*. 2019;16(5):352–8.
- Kanaan MHG. Prevalence, resistance to antimicrobials, and antibiotypes of *Arcobacter* species recovered from retail meat in Wasit Marketplaces in Iraq. *Int J One Health*. 2021;7(1):142–50.
- Noto A, Sciortino S, Cardamone C, Ciravolo C, Napoli C, Alio V, et al. Detection of *Arcobacter* spp. in food products collected from Sicilia region: a preliminary study. *Ital J Food Saf*. 2018;7(2):7171.
- Aydin F, Yağiz A, Abay S, Müştak HK, Diker KS. Prevalence of *Arcobacter* and *Campylobacter* in beef meat samples and characterization of the recovered isolates. *J Verbraucherschutz Lebensmittelsicherh*. 2020;15(1):15–25.
- Caruso M, Latorre L, Santagada G, Fraccalvieri R, Difato LM, Miccolupo A, et al. *Arcobacter* spp. in bovine milk: an emerging pathogen with potential zoonotic risk. *Ital J Food Saf*. 2018;7(4):7685.
- Mudadu AG, Melillo R, Salza S, Mara L, Marongiu L, Piras G, et al. Detection of *Arcobacter* spp. in environmental and food samples collected in industrial and artisanal sheep's milk cheese-making plants. *Food Control*. 2021;126:108100.
- Mudadu AG, Salza S, Melillo R, Mara L, Piras G, Spanu C, et al. Prevalence and pathogenic potential of *Arcobacter* spp. isolated from edible bivalve molluscs in Sardinia. *Food Control*. 2021;127:108139.
- Zhang X, Alter T, Gözl G. Characterization of *Arcobacter* spp. isolated from retail seafood in Germany. *Food Microbiol*. 2019;82:254–8.
- Chukwu MO, Abia A, Ubomba-Jaswa E, Dewar JB, Obi CL. Mixed aetiology of diarrhoea in infants attending clinics in the North-West province of South Africa: potential for sub-optimal treatment. *Pathogens*. 2020;9(3):198.
- Webb AL, Boras VF, Kruczkiewicz P, Selinger LB, Taboada EN, Inglis GD. Comparative detection and quantification of *Arcobacter butzleri* in stools from diarrheic and nondiarrheic people in Southwestern Alberta. *Canada J Clin Microbiol*. 2016;54(4):1082–8.
- Figueras MJ, Levican A, Pujol I, Ballester F, Rabada QM, Gomez-Bertomeu F. A severe case of persistent diarrhoea associated with *Arcobacter cryaerophilus* but attributed to *Campylobacter* sp. and a review of the clinical incidence of *Arcobacter* spp. *New Microb New Infect*. 2014;2(2):31–7.
- Ferreira S, Queiroz JA, Oleastro M, Domingues FC. Insights in the pathogenesis and resistance of *Arcobacter*: a review. *Crit Rev Microbiol*. 2016;42(3):364–83.
- Van den Abeele AM, Vogelaers D, Van Hende J, Houf K. Prevalence of *Arcobacter* species among humans, Belgium, 2008–2013. *Emerg Infect Dis*. 2014;20(10):1731–4.
- Mandisodza O, Burrows E, Nulsen M. *Arcobacter* species in diarrhoeal faeces from humans in New Zealand. *New Zeal Med J*. 2012;125(1353):40–6.
- Vandenberg O, Dediste A, Houf K, Ibekwem S, Souayah H, Cadranet S, et al. *Arcobacter* species in humans. *Emerg Infect Dis*. 2004;10(10):1863–7.
- Wang Y, Dong Y, Deng F, Liu D, Yao H, Zhang Q, et al. Species shift and multidrug resistance of *Campylobacter* from chicken and swine, China, 2008–14. *J Antimicrob Chemoth*. 2016;71(3):666–9.
- Ruiz De Alegría Puig C, Fernández Martínez M, Pablo Marcos D, Agüero Balbín J, Calvo Montes J. Outbreak of *Arcobacter butzleri*? An emerging enteropathogen. *Enferm Infect Micr Cl*. 2021;41(3):169–72.
- Atabay HI, Wainø M, Madsen M. Detection and diversity of various *Arcobacter* species in Danish poultry. *Int J Food Microbiol*. 2006;109(1–2):139–45.
- Aydin F, Gümüşsoy KS, Atabay HI, İça T, Abay S. Prevalence and distribution of *Arcobacter* species in various sources in Turkey and molecular analysis of isolated strains by ERIC-PCR. *J Appl Microbiol*. 2007;103(1):27–35.
- Bodhidatta L, Srijan A, Serichantalergs O, Bangtrakulnonth A, Wongstitwilairung B, McDaniel P, et al. Bacterial pathogens isolated from raw meat and poultry compared with pathogens isolated from children in the same area of rural Thailand. *Se Asian J Trop Med*. 2013;44(2):259–72.
- Collado L, Jara R, Vázquez N, Telsaint C. Antimicrobial resistance and virulence genes of *Arcobacter* isolates recovered from edible bivalve molluscs. *Food Control*. 2014;46:508–12.
- Nelapati S, Tumati SR, Thirtham MR, Ramani PR, Kamisetty AK, Ch BK. Occurrence, virulence gene and antimicrobial susceptibility profiles of *Arcobacter* sp. isolated from catla (*Catla catla*) in India. *Lett Appl Microbiol*. 2020;70(5):365–71.
- Vicente-Martins S, Oleastro M, Domingues FC, Ferreira S. *Arcobacter* spp. at retail food from Portugal: prevalence, genotyping and antibiotics resistance. *Food Control*. 2018;85:107–12.
- Patyal A, Rathore RS, Mohan HV, Dhama K, Kumar A. Prevalence of *Arcobacter* spp. in humans, animals and foods of animal origin including sea food from India. *Transbound Emerg Dis*. 2011;58(5):402–10.
- Lappi V, Archer JR, Cebelinski E, Leano F, Besser JM, Klos RF, et al. An outbreak of foodborne illness among attendees of a wedding reception in Wisconsin likely caused by *Arcobacter butzleri*. *Foodborne Pathog Dis*. 2013;10(3):250–5.
- Ramees TP, Rathore RS, Bagalkot PS, Mohan HV, Kumar A, Dhama K. Detection of *Arcobacter butzleri* and *Arcobacter cryaerophilus* in clinical samples of humans and foods of animal origin by cultural and multiplex PCR based methods. *Asian J Anim Vet Adv*. 2014;9(4):243–52.
- Merga JY, Leatherbarrow AJH, Winstanley C, Bennett M, Hart CA, Miller WG, et al. Comparison of *Arcobacter* isolation methods, and diversity of *Arcobacter* spp. in Cheshire. *United Kingdom Appl Environ Microb*. 2011;77(5):1646–50.
- Bojanić K, Midwinter AC, Marshall JC, Biggs PJ, Acke E. Isolation of emerging *Campylobacter* species in working farm dogs and their frozen home-killed raw meat diets. *J Vet Diagn Invest*. 2019;31(1):23–32.
- Engberg J, On SLW, Harrington CS, Gerner-Smidt P. Prevalence of *Campylobacter*, *Arcobacter*, *Helicobacter*, and *Sutterella* spp. in human fecal samples as estimated by a reevaluation of isolation methods for campylobacters. *J Clin Microbiol*. 2000;38(1):286–91.
- Barakat A, El-Razik K, Elfadaly HA, Rabie NS, Sadek S, Almuzaini AM. Prevalence, molecular detection, and virulence gene profiles of *Campylobacter* species in humans and foods of animal origin. *Vet World*. 2020;13(7):1430–8.
- Zhang M, Gu Y, Li Y, Ju C, Zhou G, Guo Y, et al. Interpretation for the group standards of the isolation and identification of *Campylobacter jejuni* and *Campylobacter coli*. *Chin J Epidemiol*. 2019;40(09):1052–4.

39. Yesilmen S, Vural A, Erkan ME, Yildirim IH. Prevalence and antimicrobial susceptibility of *Arcobacter* species in cow milk, water buffalo milk and fresh village cheese. *Int J Food Microbiol.* 2014;188:11–4.
40. Iwu CD, Ekundayo TC, Okoh AI. A Systematic Analysis of research on *Arcobacter*: public health implications from a food-environment interphase perspective. *Foods.* 2021;10(7):1673.
41. Venâncio I, Luís Â, Domingues F, Oleastro M, Pereira L, Ferreira S. The prevalence of *Arcobacteraceae* in aquatic environments: a systematic review and meta-analysis. *Pathogens.* 2022;11(2):244.
42. Lean IJ, Rabiee AR, Duffield TF, Dohoo IR. Invited review: use of meta-analysis in animal health and reproduction: methods and applications. *J Dairy Sci.* 2009;92(8):3545–65.
43. Lo CKL, Mertz D, Loeb M. Newcastle-Ottawa scale: comparing reviewers' to authors' assessments. *BMC Med Res Method.* 2014;14:1–5.
44. Borenstein M, Hedges LV, Higgins JPT, Rothstein HR. *Introduction to Meta-analysis.* Oxford: Wiley; 2009. <https://onlinelibrary.wiley.com/doi/book/10.1002/9780470743386>.
45. Higgins JPT, Thompson SG. Quantifying heterogeneity in a meta-analysis. *Stat Med.* 2002;21:1539–58.
46. Egger M, Smith GD, Schneider M, Minder C. Bias in meta-analysis detected by a simple, graphical test. *British Med J.* 1997;315(7109):629–34.
47. Begg CB, Mazumdar M. Operating characteristics of a rank correlation test for publication bias. *Biometrics.* 1994;50(4):1088–101.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.